

ProQinase™ CDK13/CycK

cyclin dependent kinase 13

Recombinant Human Active Protein Kinase

HGNC Symbol: CDK13

Synonyms: CDC2L, CDC2L5, CHED

Product No.: 1530-1484-1

Lot: 011

Description: Human CDK13, internal fragment amino acids P₆₅₆-G₁₀₅₀ (as in [NCBI/Protein](#) entry NP_003709.3), N-terminal GST-HIS₆ fusion protein with a 3C cleavage site and human CycK, M₁-S₃₀₀ (as in [NCBI/Protein](#) entry NP_001092872.1), N-terminally fused to GST-HIS₆ 3C cleavage site, coexpressed in Sf9 insect cells

Product identity: CDK13/CycK Lot 01, was confirmed as CDK13/CycK by mass spectrometry LC-ESI-MS/MS

Theoretical MW _{GST-CDK13} :	73831	Da
Theoretical MW _{GST-CycK} :	63031	Da

Expression host: Sf9 insect cells

Purification: GST-Affinity Chromatography

Activation: This kinase was not activated by special procedures

Storage buffer: 50 mM HEPES pH 7.5, 100 mM NaCl, 5 mM DTT, 15 mM reduced glutathione, 20 % glycerol

Storage temperature: -80°C

For complete recovery, mix well and spin before use. Product must not be stored in diluted solutions, aliquots below 10 µl are not advisable. Avoid repeated freeze-thaw cycles!

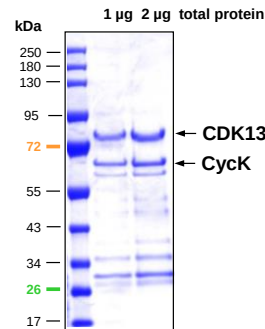
Protein concentration: 0.337 µg/µl
(Bradford method using BSA [Sigma, cat# A-7638, Lot 79H7641] as standard protein)

Biochemical Parameters:

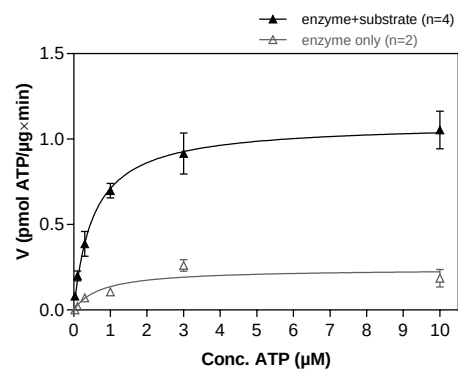
Specific kinase activity (P_i transfer): 1.1 pmol/µg*min

ATP-K_M: 0.54 µM

CDK13/CycK Lot 011:
Coomassie stain



CDK13/CycK Lot 011:
Determination of V_{max} and K_M value for ATP



- Assay conditions:
 - 60 mM HEPES-NaOH, pH 7.5
 - 3 mM MgCl₂
 - 3 mM MnCl₂
 - 3 µM Na-orthovanadate
 - 1.2 mM DTT
 - 50 µg/ml PEG_{20,000}
 - ATP (variable)
 - Substrate: SUPT5H 20 µg/ml
 - Kinase: 4 µg/ml

Assay technology:
Radiometric filter binding assay
MSFC membrane (96 well plate, Millipore)

Sequence information

GST-CDK13 Recombinant Fusion Protein Amino Acid Sequence							
1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLIERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPEML	KMFKDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPIQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHGG	RDSLEVLFGG	240
241	PPGGDDLSKS	PEEKKTATQL	HSKRRPKICG	PRYGETKEKD	IDWGRKCVDK	FDIIGIIGEG	300
301	TYGQVYKARD	KDTGEMVALK	KVRLDNEKEG	FPITAIREIK	ILRQLTHQSI	INMKEIVTDK	360
361	EDALDFKKDK	GAFFLVFEYM	DHDLMLGLES	GLVHFNNENHI	KSFMRQLMEG	LDYCHKKNFI	420
421	HRDIKCSNIL	LNNRGQIKLA	DFGLARLYSS	EESRPYTNKV	ITLWYRPPPEL	LLGEERYTPA	480
481	IDVWSCGCIL	GELFTKKPIF	QANQELAQLE	LISRICGSPC	PAVWPDVIKL	PYFNTMKPKK	540
541	QYRRKLREEF	VFIPAAALDL	FDYMLALDPS	KRCTAEQALQ	CEFLRDVEPS	KMPPPDLPLW	600
601	QDCHELWSKK	RRRQKQMGMT	DDVSTIKAPR	KDLSLG			660

1-218: GST **Red**: HIS6-tag **Green**: 3C cleavage site **blue**: CDK13 fragment

CDK13 wt ¹ Amino Acid Sequence							
1	MPSSSDTALG	GGGGLSWAEK	KLEERRKRRR	FLSPQQPPLL	LPLLQPQLLQ	PPPPPPPLLF	60
61	LAAPGTAAAA	AAAAAASSSC	FSPGPPLEVK	RLARGKRRAG	GRQKRRRGPR	AGQEAERKRV	120
121	FSLPQPQQDG	GGGASSGGGV	TPLVEYEDVS	SQSEQGLLLG	GASAATAATA	AGGTGGSGGS	180
181	PASSSGTQRR	GEGSERRPRR	DRSSSSGRSK	ERHREHRRRD	GQRGGSEASK	SRSRHSHSGE	240
241	ERAEVAKSGS	SSSSGGRRKS	ASATSSSSSS	RKDRDSKAHR	SRTKSSKEPP	SAYKEPPKAY	300
301	REDKTEPKAY	RRRRSLSPLG	GRDDSPVSHR	ASQSLRSRKS	PSPAGGGSSP	YSRRLPRSPS	360
361	PYSRRRSPSY	SRHSSYERGG	DVSPSPYSSS	SWRRSRSPYS	PVLRRSGKSR	SRSPYSSRHS	420
421	RSRSRHRLSR	SRSRHSSISP	STLTLSKSLA	AELNKNKKAR	AAEAARAAEA	AKAAEATKAA	480
481	EAAAAKAAS	NTSTPTKGNT	ETSASASQTN	HVKDVKKIKI	EHAPSPSSGG	TLKNDKAKTK	540
541	PPLQVTKVEN	NLIVDKATKK	AVIVGESKES	AATKEESVSL	KEKTKPLTPS	IGAKEKEQHV	600
601	ALVTSTLPPL	PLPPMLPEDK	EADSLRGNIS	VKAVKKEVEK	KLRCLLADLP	LPPPELPGGDD	660
661	LSKSPEEKKT	ATQLHSKRRP	KICGPRYGET	KEKDIDWGKR	CVDKFDIIGI	IGEGTYGQVY	720
721	KARDKDTGEM	VALKKVRLDN	EKEGFPITAI	REIKILRQLT	HQSIINMKEI	VTDKEDALDF	780
781	KKDKGAFFLV	FEYMDHDLMG	LLESGLVHFN	ENHIKSFMQR	LMEGLDYCHK	KNFLHRDIKC	840
841	SNILLNNRGQ	IKLADFGLAR	LYSSEESRPY	TNKVITLWYR	PELLLLGEER	YTPAIDVWSC	900
901	GCILGELFTK	KPIFQANQEL	AQLELISRIC	GSPCPAVWPD	VIKLPYFNTM	KPKKQYRRKL	960
961	REEFVFIPAA	ALDLFDYMLA	LDPSKRCTAE	QALQCEFLRD	VEPSKMPPPD	LPLWQDCHEL	1020
1021	WSKRRRRQKQ	MGMTDDVSTI	KAPRKDLSLG	LDDSRNTNPQ	GVLPSQLKS	QGSSNVAPVK	1080
1081	TGPGQHLNHS	ELAILLNLQ	SKTSVNMADE	VQVLNIKVNS	ETQQQLNKIN	LPAGILATGE	1140
1141	KQTDPTSTPQ	ESSKPLGGIQ	PSSQTIQPKV	ETDAAQAAVQ	SAFAVLLTQL	IKAQQSKQKD	1200
1201	VLEERENG	GHEASLQLRP	PPEPSTPVSG	QDDLIQHQM	RILELTPEPD	RPRILPPDQR	1260
1261	PPEPPEPPPV	TEEDLDYRTE	NQHVPTTSSS	LTDPHAGVKA	ALLQLLAHQH	PQDDPKREGG	1320
1321	IDYQAGDTYV	STSDYKDNFG	SSSFSSAPYV	SNDGLGSSSA	PPLERRSFIG	NSDIQSLDNY	1380
1381	STASSHSGGP	PQPSAFSESF	PSSVAGYGDI	YLNAGPMLFS	GDKDHRFEYS	HGPIAVLANS	1440
1441	SDPSTGPEST	HPLPAKMHNH	NYGGNLQENP	SGPSLMHGQT	WTSPAQGPY	SQGYRGHIST	1500
1501	STGRGRGRGL	PY					1560

blue: CDK13 sequence expressed in recombinant protein

¹[NCBI/Protein](https://www.ncbi.nlm.nih.gov/Protein) accession number NP_003709.3

Recombinant Proteins

GST-CycK Recombinant Fusion Protein Amino Acid Sequence

1	MSPILGYWKI	KGLVQPTRLL	LEYLEEKYEE	HLIERDEGDK	WRNKKFELGL	EFPNLPYYID	60
61	GDVKLTQSMA	IIRYIADKHN	MLGGCPKERA	EISMLEGAVL	DIRYGVSRIA	YSKDFETLKV	120
121	DFLSKLPEML	KMFKDRLCHK	TYLNGDHVTH	PDFMLYDALD	VVLYMDPMCL	DAFPKLVCFK	180
181	KRIEAIPQID	KYLKSSKYIA	WPLQGWQATF	GGGDHPPKSD	PMGHHHHHGG	RDSLEVLFGG	240
241	PMKENKENS	PSVTSANLDH	TKPCWYWDKK	DLAHTPSQLE	GLDPATEARY	RREGARFIFD	300
301	VGTRLGLHYD	TLATGIIYFH	RFYMFHSFKQ	FPRYVTGACC	LFLAGKVEET	PKCKDKIIT	360
361	ARSLNDVQF	QFGDDPKKEE	VMVLERILLQ	TIKFDLQVEH	PYQFLLKYAK	QLKGDKNKIQ	420
421	KLVMMAWTFV	NDSLCTTSL	QWEPEIIAVA	VMYLAGRLCK	FEIQEWTSKP	MYRRWWEQFV	480
481	QDVPVDVLED	ICHQILDLYS	QGKQMPHHT	PHQLQPPSL	QPTPQVPQVQ	QSQPSQSSEP	540
541	S						600

1-218: GST Red: HIS6-tag Green: 3C cleavage site blue: CycK fragment

CycK wt² Amino Acid Sequence

1	MKENKENS	SVTSANLDHT	KPCWYWDKKD	LAHTPSQLEG	LDPATEARYR	REGARFIFDV	60
61	GTRLGLHYD	LATGIIYFHR	FYMFHSFKQF	PRYVTGACCL	FLAGKVEETP	KKCKDIKTA	120
121	RSLNDVQFG	QFGDDPKKEE	VMVLERILLQ	IKFDLQVEHP	YQFLLKYAKQ	LKGDKNKIQK	180
181	LVQMAWTFVN	DSLCTTSLQ	WEPEIIAVAV	MYLAGRLCKE	EIQEWTSKPM	YRRWWEQFVQ	240
241	DVPVDVLEDI	CHQILDLYSQ	GKQMPHHTP	HQLQPPPSLQ	PTPQVPQVQQ	SQPSQSSEPS	300
301	QFQQKDPQQP	AQQQQPAQQP	KKPSPQPSSP	RQVKRAVVVS	PKEENKAAEP	PPPKIPKIET	360
361	THPPLPPAHP	PPDRKPPLAA	ALGEAEPPGP	V DATDLPKVQ	IPPPAHPAPV	HQPPPLPHRP	420
421	PPPPSSSYMT	GMSTTSSYMS	GEGYQSLQSM	MKTEGPSYGA	LPPAYGPPAH	LPYHPHVYPP	480
481	NPPPPPVPPP	PASFPPPAIP	PPTPGYPPPP	PTYNPNFPPP	PPRLPPTHAV	PPHPPPGGLGL	540
541	PPASYPPPAV	PPGGQPPVPP	PIPPPGMPPV	GGLGRAAWMR			600

blue: CycK sequence expressed in recombinant protein

¹NCBI/Protein accession number NP_001092872.1

HGNC identifier CycK: CCNK

Recombinant Proteins